SEQUENCE LISTING

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							ctg Leu 40									144	
atg Met	gac Asp 50	ctg Leu	cgc Arg	ctg Leu	gac Asp	cac His 55	cag Gin	ttc Phe	tca Ser	ctg Leu	cct Pro 60	gtg Val	gca Ala	gag Glu	ccg Pro	192	
							cag Gin									240	
							atc lle									288	
							cac His									336	
							gcc Ala 120									384	
							agg Arg									432	
							ctg Leu									480	
							agc Ser	Thr								528	
							aag Lys									576	
cac	tgc	att	tcc	agc	gac	cct	cgc	tac	tgg	tac	ggg	aaa	acg	cag	cac	624	

His	Cys	11e		Ser	Asp	Pro	Arg 200		Trp	Tyr	Gly	Lys 205			His	
ag1 Ser	Ser 210	Leu	gac Asp	cag Gin	agt Ser	Ser 215	Pro	occ Pro	cag Gin	agc Ser	gga Gly 220	Val	tcg Ser	acc Thr	tcc Ser	672
	Asn					Gly					Lys				Pro 240	720
ctt Leu	agg Arg	aaa Lys	aca Thr	got Ala 245	Ser	gaa Glu	ccg Pro	aat Asn	ctg Leu 250	Lys	tta Leu	cgg Arg	tcc Ser	agg Arg 255	cta Leu	768
	cag Gin			Āla					Ser					Arg	aaa Lys	816
	ggg Gly		Val					Lys							aca Thr	864
gac Asp	tcc Ser 290	Ala	tgc Cys	agc Ser	agc Ser	gcc Ala 295	cca Pro	ggc Gly	tcc Ser	gga Gly	ccc Pro 300	Ser	tca Ser	ccc Pro	aac Asn	912
aac Asn 305	agc Ser	tcc Ser	ggg Gly	agc Ser	gtc Val 310	agc Ser	gcg Ala	gag Glu	aac Asn	ggt Gly 315	atc Ile	gcg Ala	ccc Pro	gcc Ala	gtc Val 320	960
	agc Ser															1008
	ggc Gly															1056
	atc lle															1104
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ctc Leu 385	tcc Ser	ctt Leu	ttc Phe	ccc Pro	ggc Gly 390	acc Thr	cac His	ctc Leu	act Thr	ccc Pro 395	tac Tyr	ctg Leu	agc Ser	acc Thr	tog Ser 400	1200
ccc Pro	ttg Leu	gag Glu	cgg Arg	gac Asp 405	gga Gly	ggg Gly	gca Ala	gcg Ala	cac His 410	agc Ser	cct Pro	ctt Leu	ctg Leu	cag Gin 415	cac His	1248
	gtc Val															1296
	gga Gly															13 44
	tcc Ser 450															1392
	cag Gin															1440
	atc lle							Phe								1488

									•				005	0		
				ı Glr					1 Lys					g cc	a agc o Ser	1536
			Are					His					Gli		g gag u Glu	1584
		Glu					Leu					Leu			g ctg g Leu	1632
	Gly					His					Val				cag Gln 560	1680
					Asp					Glu						1728
				Arg					Gin					Are	cag Gln	1776
			Leu										Arg		tac Tyr	1824
		Ser								gtg Val		Phe			cac His	1872
										gcg Ala 635						1920
										agg Arg						1968
										tgc Cys						2016
										cag Gin						2064
										gag Glu						2112
										cac His 715						2160
										cag Gin						2208
							Ser			gtc Val						2256
Gly	Val	Gly 755	Val	Asp	Ser	Asp	Thr 7 60	lle	Trp	aac Asn	Glu	Va I 765	His	Ser	Ala	2304
Gly	gca Ala 770	gcc Ala	cgc Arg	ctg Leu	Ala	gtg Val 775	ggc	tgc Cys	gtg Val	gta Val	gag Glu 780	ctg Leu	gtc Val	ttc Phe	aag Lys	2352
gtg Val 785	gcc Ala	aca Thr	ggg Giy	Glu	ctg Leu 790	aag a Lys <i>i</i>	aat , Asn (ggc Gly	Phe	gct Ala 795	gtg Vai	gtc Val	ogo Arg	ccc Pro	cct Pro 800	2400

gg Gi	a ca y Hi	c ca s Hi	t gcg s Ala	g gag a Glu 805	ı Glı	g ago u Ser	ac _t Thi	g cco	atg Met 810	Gly	tt Pho	t tge в Суз	s tac s Ty	c tto r Pho 81!	c aac e Asn 5	2448
to Se	c gt r Va	g gc I Al	c gtg a Val 820	Ala	g gco	aag Lys	ct1	t ctg Let 825	Glr	cag Glr	agi Ari	g ttg g Lei	ago Sei 830	- Va	g agc I Ser	2496
aa; Ly:	g ate	c ct e Le 83	u He	gtg Val	gac Asp	tgg Trp	gac Asp 840	Val	cac His	cat His	gga	a aad / Asr 845	Gly	g acc	cag Gln	2544
Gli	g gc n Ala 850	a Pho	c tac e Tyr	ago Ser	gac Asp	cct Pro 855	Ser	gto Val	ctg Leu	tac Tyr	Met 860	: Ser	Cto Leu	cac His	cgc Arg	2592
tad Tyr 865	As	gat Asp	t ggg o Gly	aac Asn	tto Phe 870	Phe	cca Pro	ggo	agc Ser	ggg Gly 875	Ala	cct Pro	gat Asp	gag Glu	gtg Val 880	2640
ggo Gly	aca Thr	ggg Gly	ccc Pro	ggc Gly 885	gtg Vai	ggt Gly	ttc Phe	aac Asn	gtc Val 890	Asn	atg Met	gct Ala	tto Phe	acc Thr 895	Gly	2688
ggo Gly	ctg Leu	gac Asp	Pro 900	ccc Pro	atg Met	gga Gly	gac Asp	gct Ala 905	gag Glu	tac Tyr	ttg Leu	gcg	gcc Ala 910	Phe	aga Arg	2736
acg Thr	gtg Vai	Val 915	atg Met	ccg Pro	atc Ile	gcc Ala	agc Ser 920	gag Glu	ttt Phe	gcc Ala	ccg Pro	gat Asp 925	gtg Val	gtg Val	ctg Leu	2784
gtg Val	tca Ser 930	Ser	ggc	ttc Phe	gat Asp	gcc Ala 935	gtg Val	gag Glu	ggc Gly	cac His	ccc Pro 940	Thr	cct Pro	ctt Leu	ggg Gly	2832
ggc Gly 945	tac Tyr	aac Asn	ctc Leu	tcc Ser	gcc Ala 950	aga Arg	tgc Cys	ttc Phe	ggg Gly	tac Tyr 955	ctg Leu	acg Thr	aag Lys	cag Gin	ctg Leu 960	2880
atg Met	ggc Gly	ctg Leu	gct Ala	ggc Gly 965	ggc Gly	cgg Arg	att Ile	gtc Val	ctg Leu 970	gcc Ala	ctc Leu	gag Glu	gga Gly	ggc Gly 975	cac His	2928
gac Asp	ctg Leu	acc Thr	gcc Ala 980	att He	tgc Cys	gac Asp	gcc Ala	tcg Ser 985	gaa Glu	gca Ala	tgt Cys	gtt Val	tct Ser 990	gcc Ala	ttg Leu	2976
ctg Leu	gga Gly	aac Asn 995	gag Glu	ctt Leu	gat Asp	Pro	ctc Leu 1000	Pro	gaa Glu	aag Lys	gtt Val	tta Leu 1005	Gln	caa Gin	aga Arg	3024
ccc Pro	aat Asn 1010	Ala	aac Asn	gct Ala	Val	cgt Arg 1015	tcc Ser	atg Met	gag Glu	Lys	gtc Val 020	atg Met	gag Glu	atc Ile	cac His	3072
agc Ser 1025	Lys	tac Tyr	tgg Trp	Arg	tgc Cys 1030	Leu (cag Gln	cgc Arg	Thr	acc Thr 1035	Ser	aca Thr	gcg Ala	ggg Gly	cgt Arg 1040	3120
tct Ser	ctg Leu	atc IIe	gag Giu	gct Ala 1045	cag Gln	act 1 Thr (tgc Cys	Glu .	aac Asn 1050	gaa ; Glu (gaa Glu	gcc Ala	Glu	acg Thr 1055	Val	3168
acc Thr	gcc Ala	atg Met	gcc Ala 1060	tog (Ser l	ctg Leu :	tcc g Ser \	/al I	ggc Gly 1065	gtg a Val i	aag (Lys I	ecc Pro	Ala 🛚	gaa Glu 1070	aag Lys	aga Arg	3216
cca Pro	Asp	gag Glu 1075	gag d Glu l	occ a Pro I	atg (Glu G	gag Glu (1080	gag (Glu l	ocg (Pro l	ecc o Pro l	etg Leu	tag				3255

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- ₹212> PRT
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<400> 2

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Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val 20 25 30

Asp Val Ala Thr Ala Leu Pro Leu Gin Val Ala Pro Ser Ala Val Pro 35 40 45

Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro 50 60

Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln 65 75 80

Lys Gin Gin He Gin Arg Gin He Leu He Ala Giu Phe Gin Arg Gin 85 90 95

His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile . 100 105 110

Lys Gin Gin Giu Met Leu Ala Met Lys His Gin Gin Giu Leu Leu 115 120 125

Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu 130 135 140

Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys 145 155 160

Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln 165 170 175

Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn 180 185 190

His Cys IIe Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His 195 200 205

Ser Ser Leu Asp Gin Ser Ser Pro Pro Gin Ser Gly Val Ser Thr Ser 210 215 220

Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro 225 230 240

Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu 245 250 255

Lys Gin Lys Val Ala Giu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys 260 265 270

Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr 275 280 285

Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn 290 295 300

Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val 305 310 320

Pro Ser IIe Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg 325 330 335

Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340 345 350

Asn lle Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355 360 365

Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg

Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385 395 400 Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His 405 410 415 Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
420 425 430 Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg 435 440 445 Val Ser Pro Ser IIe His Lys Leu Arg Gln His Arg Pro Leu Gly Arg 450 455 460 Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu 465 470 475 480 Val lle Gin Gin His Gin Gin Phe Leu Giu Lys His Lys Gin Gin 485 490 495 Phe Gin Gin Gin Leu Gin Met Asn Lys IIe IIe Pro Lys Pro Ser 500 505 510 Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu 515 520 525 Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530 540 Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545 550 555 560 Glu Pro IIe Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val 565 570 575 Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590 Gln Ala Leu Leu Glu Gln Gln Arg IIe His Gln Leu Arg Asn Tyr 595 600 605 Gin Ala Ser Met Giu Ala Ala Giy ile Pro Val Ser Phe Giy Giy His 610 615 620 Arg Pro Leu Ser Arg Ala Gin Ser Ser Pro Ala Ser Ala Thr Phe Pro 625 630 635 640 Val Ser Val Gin Giu Pro Pro Thr Lys Pro Arg Phe Thr Thr Giy Leu 645 650 655 Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser 660 665 670 Ser Ser His Pro Glu His Ala Gly Arg IIe Gln Ser IIe Trp Ser Arg 675 680 685 Leu Gin Giu Thr Giy Leu Arg Giy Lys Cys Giu Cys Iie Arg Giy Arg 690 695 700 Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr 705 710 715 720 Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys 725 730 735 Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly 740 745 750 Gly Val Gly Val Asp Ser Asp Thr IIe Trp Asn Glu Val His Ser Ala 755 760 765 Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys

770

Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro

775

Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn 805 810 815

Ser Val Ala Val Ala Ala Lys Leu Leu Gin Gin Arg Leu Ser Val Ser

Lys lle Leu lle Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln 835 840 845

Gin Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg 850 855 860

Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val 865 870 875 880

Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly 885 890 895

Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900 905 910

Thr Val Val Met Pro Ile Ala Ser Giu Phe Ala Pro Asp Val Val Leu 915 920 925

Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly 930 935 940

Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu 945 950 955 960

Met Gly Leu Ala Gly Gly Arg fle Val Leu Ala Leu Glu Gly Gly His 965 970 975

Asp Leu Thr Ala IIe Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 980 985 990

Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg

Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His 1015

Ser Lys Tyr Trp Arg Cys Leu Gin Arg Thr Thr Ser Thr Ala Gly Arg 1025 1030 1035 1046

Ser Leu lle Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val

Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg 1060 1065 1070

Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu

<210>

3255

〈211〉 〈212〉 DNA

⟨213⟩ Artificial

〈220〉

〈221〉 CDS **〈222〉**

(1).. (3255) Dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

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															ccc Pro	144
															ccg Pro	192
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															cag Gln	288
			ctc Leu 100	Ser					Ala					His	atc	336
			Gln												ctg Leu	384
		Gin	cgg Arg													432
	GIn		ogg Arg													480
			agt Ser													528
gaa Glu	ttt Phe	gtc Val	ctc Leu 180	aat Asn	aaa Lys	aag Lys	aag Lys	gcg Ala 185	ctg Leu	gcc Ala	cac His	cgg Arg	aat Asn 190	ctg Leu	aac Asn	576
			tcc Ser													624
			gac Asp													672
			ccg Pro													720
			aca Thr													768
			gtg Val 260				Arg					Leu				816
			gtg Val			Ala					Pro					864
			tgc Cys		Ser					Gly						912
aac Asn	agc Ser	tcc Ser	ggg Gly	agc Ser	gtc : Val	agc (Ser /	gcg Ala	gag Glu	aac Asn	ggt a Gly	atc lle	gcg Ala	ccc Pro	gcc Ala	gtc Val	960

			09598	
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ccc agc atc Pro Ser IIe	ccg gcg gag ac Pro Ala Glu Th 325	g agt ttg gcg r Ser Leu Ala 330	cac aga ctt gtg g His Arg Leu Val A 33	ca cga 1008 Ia Arg 35
gaa ggc tcg Glu Gly Ser	gcc gct cca ct Ala Ala Pro Le 340	t ccc ctc tac u Pro Leu Tyr 345	aca tcg cca tcc t Thr Ser Pro Ser Lo 350	tg ccc 1056 eu Pro
aac atc acg Asn lle Thr 355	ctg ggc ctg cc Leu Gly Leu Pr	t gcc acc ggc o Ala Thr Gly 360	ccc tct gcg ggc ac Pro Ser Ala Gly Th 365	eg gog 1104 or Ala
ggc cag cag Gly Gln Gln 370	gac acc gag ag Asp Thr Glu Ar 37	g Leu Thr Leu	ccc gcc ctc cag ca Pro Ala Leu Gin Gi 380	ng agg 1152 n Arg
ctc tcc ctt Leu Ser Leu 385	ttc ccc ggc ac Phe Pro Gly The 390	c cac ctc act r His Leu Thr	ccc tac ctg agc ac Pro Tyr Leu Ser Th 395	c tcg 1200 ir Ser 400
ccc ttg gag Pro Leu Glu	cgg gac gga gg Arg Asp Gly Gly 405	g gca gcg cac y Ala Ala His 410	agc cct ctt ctg ca Ser Pro Leu Leu GI 41	n His
Met Val Leu I	ctg gag cag cca Leu Glu Gln Pro 420	a ccg gca caa o Pro Ala Gin 425	gca ccc ctc gtc ac Ala Pro Leu Val Th 430	a ggc 1296 r Gly
ctg gga gca d Leu Gly Ala i 435	ctg ccc ctc cac Leu Pro Leu His	gca cag tcc Ala Gin Ser 440	ttg gtt ggt gca ga Leu Val Gly Ala As 445	c cgg 1344 p Arg
gtg tcc ccc 1 Val Ser Pro S 450	tcc atc cac aag Ser lle His Lys 455	Leu Arg Gin	cac cgc cca ctg gg His Arg Pro Leu Gl 460	g ogg 1392 y Arg
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gtc atc cag o Val lie Gin G	cag cag cat cag Gin Gin His Gin 485	cag ttt ctg Gin Phe Leu 490	gag aaa cac aag ca Glu Lys His Lys Gir 495	Gln
Phe Gin Gin G	ag caa ctg cag iin Gin Leu Gin i00	atg aac aag a Met Asn Lys 505	atc atc ccc aag cca lle lle Pro Lys Pro 510	agc 1536 Ser
gag cca gcc c Glu Pro Ala A 515	gg cag ccg gag arg Gin Pro Giu	agc cac ccg (Ser His Pro (520	gag gag acg gag gag Blu Glu Thr Glu Glu 525	gag 1584 Glu
ctc cgt gag c Leu Arg Glu H 530	ac cag gct ctg lis Gln Ala Leu 535	ctg gac gag o Leu Asp Glu F	cc tac ctg gac cgg Pro Tyr Leu Asp Arg 540	ctg 1632 Leu
ccg ggg cag a Pro Gly Gin Ly 545	ag gag gcg cac ys Glu Ala His 550	Ala Gin Ala 🤅	gc gtg cag gtg aag ily Val Gin Val Lys 55	cag 1680 Gln 560
gag ccc att ga Glu Pro lle G	ag agc gat gag lu Ser Asp Glu 565	gaa gag gca g Glu Glu Ala 6 570	ag ccc cca cgg gag lu Pro Pro Arg Giu 575	gtg 1728 Val
Glu Pro Gly G	ag cgc cag ccc In Arg Gin Pro 80	agt gag cag g Ser Glu Gln G 585	ag ctg ctc ttc aga Iu Leu Leu Phe Arg 590	cag 1776 Gln
caa gcc ctc ct Gin Ala Leu Le 595	eu Leu Glu Gin	cag cgg atc c Gin Arg lie H 600	ac cag ctg agg aac is GIn Leu Arg Asn 605	tac 1824 Tyr
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GI	n Al 61		er Me	t GI	u Al	a Al. 61		y II	e Pr	o Va	Se 62		e GI	y Gi	y His	
	g Pr					a Gli					a Se				c ccc e Pro 640	
gt. Va	g tc I Se	t gt r Va	g ca il Gi	g ga n Gl 64	u Pr	c cco o Pro	t ace	caa, rLya	g cci s Pro 650	o Arg	g tte g Phe	c ac e Th	g ac r Th	a gg r Gi 65	c ctc y Leu 5	1968
gt: Va	g ta I Ty	t ga r As	c ac p Th 66	r Le	g atı	g ctg t Lei	g aag	g cad s His 665	s Glr	tgo Cys	ace The	c tge	c gg s Gl:	y Se	t agc r Ser	2016
ago Sei	c age	c ca r Hi 67	s Pr	c gag o Gli	g cad	s Ala	ggg Gly 680	/ Are	g ato	cag Glr	ago Ser	e ato 110 685	Tr	g to Se	c cgc r Arg	2064
cts Lei	GII GII 690	n GI	g ac	g ggo r Gly	cto Lei	c cgg I Arg 695	Gly	aaa Lys	tgo Cys	gag Glu	tgo Cys 700	5 E	c cgo Arg	g Gly	a cgc y Arg	2112
Lys 705	Ala	a Th	r Lei	ı Glu	710	ı Leu)	Gin	Thr	· Val	His 715	Ser	Glu	ı Ala	a Hia	acc Thr 720	2160
cto Leu	ctg Leu	ta Ty	t ggo r Gly	acg Thr 725	: Asr	ccc Pro	cto Leu	aac Asn	cgg Arg 730	Gin	aaa Lys	ctg Leu	gac Asp	agt Ser 735	aag Lys	2208
				Ser					Phe					Cys	ggt	2256
Gly	Val	Gly 755	Val	Asp	Ser	Asp	Thr 760	lle	Trp	Asn	Glu	Va l 765	His	Ser	gcg	2304
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gtg Val 785	gcc Ala	aca Thr	ggg	gag Glu	ctg Leu 790	aag Lys	aat Asn	ggc Gly	ttt Phe	gct Ala 795	gtg Vai	gtc Val	cgc Arg	ccc Pro	cct Pro 800	2400
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Ser	Val	Ala	Val 820	Ala	Ala	Lys	Leu	Leu 825	GIn	GIn	Arg	Leu	Ser 830	Val	Ser	2496
aag Lys	atc ile	ctc Leu 835	atc e	gtg Val	gac Asp	tgg Trp	gac Asp 840	gtg Val	cac His	cat His	gga Giy	aac Asn 845	ggg Gly	acc Thr	cag Gin	2544
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tac Tyr 865	gac Asp	gat Asp	ggg Gly	aac Asn	ttc Phe 870	ttc Phe	cca Pro	ggc Gly	Ser	ggg Gly 875	gct Ala	cct Pro	gat Asp	gag Glu	gtg Val 880	2640
ggc Gly	aca Thr	ggg Gly	ccc Pro	ggc Gly 885	gtg Val	ggt Gly	ttc Phe	Asn	gtc Val 890	aac Asn	atg Met	gct Ala	ttc Phe	acc Thr 895	ggc Gly	2688
ggc Gly	ctg Leu	gac Asp	ccc Pro 900	ccc Pro	atg Met	gga Gly	Asp .	gct Ala 905	gag Glu	tac Tyr (ttg Leu	Ala	gcc Ala 910	ttc Phe	aga Arg	2736

09598	
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ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu 945 950 955 960	2880
atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His 965 970 975	2928
gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg Asp Leu Thr Ala lle Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 980 985 990	2976
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg 995 1000 1005	3024
ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu lie His 1010 1015 1020	3072
agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg tct ctg Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg 1025 1030 1035 1040	3120
tot ctg atc gag got cag act tgc gag aac gaa gaa gcc gag acg gtc Ser Leu ile Glu Ala Gin Thr Cys Glu Asn Glu Glu Ala Glu Thr Val 1045 1050 1055	3168
acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg 1060 1065 1070	3216
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Asp Val Ala Thr Ala Leu Pro Leu Gin Val Ala Pro Ser Ala Val Pro 35 40 45	
Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro 50 55 60	
Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln 65 70 75 80	
Lys Gin Gin ile Gin Arg Gin ile Leu ile Ala Giu Phe Gin Arg Gin 85 90 95	
His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His IIe 100 105 110	

- Lys Gin Gin Giu Met Leu Ala Met Lys His Gin Gin Giu Leu Leu 115 120 125
- Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu 130 135 140
- Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys 145 155 160
- Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln 165 170 175
- Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn 180 185 190
- His Cys IIe Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His 195 200 205
- Ser Ser Leu Asp Gin Ser Ser Pro Pro Gin Ser Gly Val Ser Thr Ser 210 215 220
- Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro 225 230 235 240
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- Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn 290 295 300
- Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly IIe Ala Pro Ala Val 305 310 315 320
- Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg 325 330 335
- Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340 345 350
- Asn IIe Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355 360 365
- Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg 370 375 380
- Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385 390 395 400
- Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His 405 410 415
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- Thr Gin Ser Ala Pro Leu Pro Gin Asn Ala Gin Ala Leu Gin His Leu 465 470 475 480
- Val lie Gin Gin His Gin Gin Phe Leu Giu Lys His Lys Gin Gin 485 490 495
- Phe Gin Gin Gin Leu Gin Met Asn Lys lie lie Pro Lys Pro Ser 500 505 510

- Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu 515 520 525
- Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530 535 540
- Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545 555 560
- Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val 565 570 575
- Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590
- Gln Ala Leu Leu Glu Gln Gln Arg I le His Gln Leu Arg Asn Tyr 595 600 605
- Gin Ala Ser Met Giu Ala Ala Giy ile Pro Val Ser Phe Giy Giy His 610 615 620
- Arg Pro Leu Ser Arg Ala Gin Ser Ser Pro Ala Ser Ala Thr Phe Pro 625 630 635
- Val Ser Val Gin Giu Pro Pro Thr Lys Pro Arg Phe Thr Thr Giy Leu 645 650 655
- Val Tyr Asp Thr Leu Met Leu Lys His Gin Cys Thr Cys Gly Ser Ser 660 665 670
- Ser Ser His Pro Glu His Ala Gly Arg IIe Gln Ser IIe Trp Ser Arg 675 680 685
- Leu Gin Giu Thr Giy Leu Arg Giy Lys Cys Giu Cys Ile Arg Giy Arg 690 695 700
- Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr 705 710 715 720
- Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys 725 730 735
- Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly 740 745 750
- Gly Val Gly Val Asp Ser Asp Thr lle Trp Asn Glu Val His Ser Ala 755 760 765
- Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys 770 775 780
- Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro 785 790 795 800
- Gly Lys Leu Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn 805 810 815
- Ser Val Ala Val Ala Lys Leu Gin Gin Arg Leu Ser Val Ser 820 825 830
- Lys lle Leu lle Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln 835 840 845
- Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg 850 855 860
- Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val 865 870 875 880
- Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly 885 890 895
- Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900 905 910

Thi	- Va	1 Va 91		t Pro	0 11	e Ala	a Se 92		J Pho	e Ala	a Pr	o As 92		l Va	l Leu	ı	
Va	93		r GI:	y Pho	e A sı	93!		l Glu	ı Giy	y His	s Pro 94	_	r Pr	o Le	u Gly	,	
Gly 945		r Ası	n Le	u Sei	r Ala 950		g Cy:	s Phe	Gly	7 Ty:		u Th	r Ly	s Gl	n Let 960		
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Asp	Lei	ı Thi	986		e Cys	s Asp	Ala	985		ı Ala	а Су:	s Va	99		a Leu	ı	
Leu	Gly	/ Asi 99!		ı Leu	ı Asp	Pro	Let 100		Glu	ı Lys	s Va		u Gii 005	n Gli	n Arg		
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410

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His	Glu	GIn	Leu 100	Ser	Arg	GIn	His	G I u 105	Ala	GIn	Leu	His	Glu 110	His	lle			
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His	Cys	l le 195	Ser	Ser	Asp	Pro	Arg 200	Tyr	Trp	Tyr	Gly	Lys 205	Thr	GIn	His			
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Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr 275 280 285

Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn 290 295 300

Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly IIe Ala Pro Ala Val 305 310 315 320

Pro Ser IIe Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg 325 330 335

Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340 345 350

Asn IIe Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355 360 365

Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg 370 375 380

Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385 395 400

Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His 405 410 415

Met Val Leu Leu Glu Gin Pro Pro Ala Gin Ala Pro Leu Val Thr Giy 420 425 430

Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg 435 440 445

Val Ser Pro Ser 11e His Lys Leu Arg Gln His Arg Pro Leu Gly Arg 450 455 460

Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu 465 470 475 480

Val lle Gin Gin His Gin Gin Phe Leu Giu Lys His Lys Gin Gin 485 490 495

Phe Gin Gin Gin Leu Gin Met Asn Lys IIe IIe Pro Lys Pro Ser 500 505 510

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Leu Arg Glu His Gin Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530 540

Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545 550 555 560

Glu Pro IIe Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val 565 570 575

Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590

Gin Ala Leu Leu Giu Gin Gin Arg lie His Gin Leu Arg Asn Tyr 595 600 605

Gin Ala Ser Met Giu Ala Ala Giy IIe Pro Val Ser Phe Giy Giy His 610 615 620

Arg Pro Leu Ser Arg Ala Gin Ser Ser Pro Ala Ser Ala Thr Phe Pro 625 630 635 640

Val Ser Val Gin Giu Pro Pro Thr Lys Pro Arg Phe Thr Thr Giy Leu 645 650 655

Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser 660 665 670

Ser Ser His Pro Glu His Ala Gly Arg IIe Gln Ser IIe Trp Ser Arg 675 680 685

Leu Gin Giu Thr Giy Leu Arg Giy Lys Cys Giu Cys Ile Arg Giy Arg 690 695 700

Lys Ala Thr Leu Glu Glu Leu Gln Thr Vai His Ser Glu Ala His Thr 705 710 715 720

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Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900 905 910

Thr Val Val Met Pro IIe Ala Ser Glu Phe Ala Pro Asp Val Val Leu 915 920 925

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Asp Leu Thr Ala IIe Cys Asp Ala Ser Glu Ala Cys Vai Ser Ala Leu 980 985 990

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									gct Ala							534
									tac Tyr							582
cat His	gga Gly	gat Asp	ggt Gly	gta Val 185	gaa Glu	gac Asp	gca Ala	ttc Phe	agt Ser 190	ttc Phe	acc Thr	tcc Ser	aaa Lys	gtc Val 195	atg Met	630
acc Thr	gtg Val	tcc Ser	ctg Leu	cac His	aaa Lys	ttc Phe	tcc Ser	cca Pro	gga Gly	ttt Phe	ttc Phe	cca Pro	gga Gly	aca Thr	ggt Gly	678

gac gtg tct gat gtt ggc cta ggg aag gga cgg tac tac agt gta aat Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn 215 220 225 726 gtg ccc att cag gat ggc ata caa gat gaa aaa tat tac cag atc tgt Val Pro lle Gln Asp Gly lle Gln Asp Glu Lys Tyr Tyr Gln lle Cys 774 gaa agt gta cta aag gaa gta tac caa gcc ttt aat ccc aaa gca gtg Glu Ser Val Leu Lys Glu Val Tyr Gin Ala Phe Asn Pro Lys Ala Val 245 250 260 822 250 gtc tta cag ctg gga gct gac aca ata gct ggg gat ccc atg tgc tcc Val Leu Gin Leu Giy Ala Asp Thr IIe Ala Giy Asp Pro Met Cys Ser 265 270 275 870 ttt aac atg act cca gtg gga att ggc aag tgt ctt aag tac atc ctt Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu 918 caa tgg cag ttg gca aca ctc att ttg gga gga gga ggc tat aac ctt Gin Trp Gin Leu Ala Thr Leu lie Leu Gly Gly Gly Gly Tyr Asn Leu 295 300 305966 gcc aac acg gct cga tgc tgg aca tac ttg acc ggg gtc atc cta ggg Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly Val IIe Leu Gly 310 315 320 1014 aaa aca cta too tot gag ato cca gat cat gag ttt tto aca gca tat Lys Thr Leu Ser Ser Glu lle Pro Asp His Glu Phe Phe Thr Ala Tyr 1062 ggt cct gat tat gtg ctg gaa atc acg cca agc tgc cgg cca gac cgc Gly Pro Asp Tyr Val Leu Glu lle Thr Pro Ser Cys Arg Pro Asp Arg 1110 345 aat gag ccc cac cga atc caa caa atc ctc aac tac atc aaa ggg aat 1158 Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn 365 ctg aag cat gtg gtc tag ttgacagaaa gagatcaggt ttccagagct Leu Lys His Val Val 375 1206 gaggagtggt gcctataatg aagacagcgt gtttatgcaa gcagtttgtg gaatttgtga 1266 1326 ctgcagggaa aatttgaaag aaattacttc ctgaaaattt ccaaggggca tcaagtggca gotggottoc tggggtgaag aggcaggcac cocagagtoc tcaactggac ctaggggaag 1386 aaggagatat cccacattta aagttottat ttäaaaaaaac acacacaca aaatgaaatt 1446 tttaatottt gaaaattatt tttaagogaa ttggggaggg gagtatttta atoatottaa 1506 atgaaacaga tcagaagctg gatgagagca gtcaccagtt tgtagggcag gaggcagctg 1566 1626 agaggcaggg tttgggcctc aggaccatcc aggtggagcc ctgggagaga gggtactgat 1686 cagcagactg ggaggtgggg agaagtccgc tggtgttgtt ttagtgttat atatctttgg

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Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met 50 60

Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln 65 70 75 80

Lys Val Ser Gin Glu Gly Asp Asp Asp His Pro Asp Ser ile Glu Tyr 85 90 95

Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala 100 105 110

Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp 115 120 125

Gly Met Cys Lys Val Ala lle Asn Trp Ser Gly Gly Trp His His Ala 130 135 140

Lys Lys Asp Giu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu 145 150 160

Gly lie Leu Arg Leu Arg Arg Lys Phe Glu Arg lie Leu Tyr Val Asp 165 170 175

Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr 180 185 190

Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe 195 200 205

Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr 210 215 220

Tyr Ser Val Asn Val Pro IIe Gin Asp Giy IIe Gin Asp Giu Lys Tyr 225 230 235 240

Tyr Gln IIe Cys Glu Ser Val Leu Lys Glu Vai Tyr Gln Ala Phe Asn 245 250 255

Pro Lys Ala Val Val Leu Gin Leu Giy Ala Asp Thr lie Ala Giy Asp 260 265 270

Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly lle Gly Lys Cys Leu 275 280 285

Lys Tyr lle Leu Gin Trp Gin Leu Ala Thr Leu ile Leu Giy Giy Giy 290 295 300

Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly 305 310 315 320

Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu IIe Thr Pro Ser Cys 340 345

Arg Pro Asp Arg Asn Glu Pro His Arg IIe Gln Gln IIe Leu Asn Tyr 355 360 365

lle Lys Gly Asn Leu Lys His Val Val

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			gga Gly 20												cct Pro		96
cac His	cga Arg	atc ile 35	ogc Arg	atg Met	act Thr	cat His	aat Asn 40	ttg Leu	ctg Leu	ctc Leu	aac Asn	tat Tyr 45	ggt Gly	ctc Leu	tac Tyr		144
			gaa Glu														192
			cac His														240
			atg Met														288
			tgt Cys 100														336
			ggt Gly													;	384
			gct Ala													•	432
			tct Ser													•	480
ctg Leu	gaa Glu	ctg Leu	cta Leu	aag Lys 165	tat Tyr	cac His	cag Gin	Arg	gtg Val 170	ctg Leu	tac Tyr	att He	gac Asp	att lle 175	gat Asp	ŧ	528
att He	cac His	cat His	ggt Gly 180	gac Asp	ggc G y	gtg Val	Glu	gag Glu 185	gcc Ala	ttc Phe	tac Tyr	acc Thr	acg Thr 190	gac Asp	cgg Arg		576

gto Va	ate Med	g act t Thr 195	' Val	g too Ser	ttt Phe	cat His	aag Lys 200	Tyr	gga	a gag	tac i Tyr	tto Phe 205	? Pro	a gga o Gly	a act y Thr	624
		Leu					Ala					Tyr			t gtt a Val	672
	Tyr					Gly					ı Ser				att alle 240	720
tto Phe	aag Lys	ccg Pro	gto Val	atg Met 245	: Ser	aaa Lys	gta Val	atg Met	gag Glu 250	Met	tto Phe	cag Gin	cct Pro	ag1 Ser 255	gcg Ala	768
				Cys					Leu					: Leu	ggt Gly	816
			Leu										Glu		gtc Val	864
aag Lys	agc Ser 290	Phe	aac Asn	ctg Leu	cct Pro	atg Met 295	ctg Leu	atg Met	ctg Leu	gga Gly	ggc Gly 300	Gly	ggt Gly	tac Tyr	acc Thr	912
	Arg														ctg Leu 320	960
		gag Glu			Asn										Tyr	1008
		cca Pro														1056
		acg Thr 355														1104
		aga Arg														1152
cct Pro 385	gag Glu	gac Asp	gcc Ala	atc Ile	cct Pro 390	gag Glu	gag Glu	agt Ser	ggc Gly	gat Asp 395	gag Glu	gac Asp	gaa Glu	gac Asp	gac Asp 400	1200
		aag Lys														1248
gag Glu	gaa Glu	gag Glu	ttc Phe 420	tcc Ser	gat Asp	tct Ser	gaa Glu	gag Glu 425	gag Glu	gga Gly	gag Glu	ggg Gly	ggc Gly 430	cgc Arg	aag Lys	1296
aac Asn	tct Ser	tcc Ser 435	aac Asn	ttc Phe	aaa Lys	Lys	gcc Ala 440	aag Lys	aga Arg	gtc Val	Lys	aca Thr 445	gag Glu	gat Asp	gaa Glu	13 44
Lys		aaa Lys			Glu					۷a۱						1392
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Arg Lys Met Glu lle Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met 50 60

Thr Lys Tyr His Ser Asp Asp Tyr IIe Lys Phe Leu Arg Ser IIe Arg 65 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val 85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gin Leu 100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln 115 120 125

Thr Asp IIe Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp IIe Val Leu Ala IIe 145 150 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr lle Asp 11e Asp 175

lle His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg 180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr 195 200 205

Gly Asp Leu Arg Asp IIe Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val 210 215 220

Asn Tyr Pro Leu Arg Asp Gly IIe Asp Asp Glu Ser Tyr Glu Ala IIe 225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 245 250 255

Val Val Leu Gin Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly 260 265 270

^{(211) 482}

Cys	Phe	275		Thr	lle	Lys	Gly 280		Ala	Lys	Cys	Va I 285		ı Ph∈	Val			
Lys	Ser 290	Phe	Asn	Leu	Pro	Met 295		Met	Leu	Gly	Gly 300	-	Gly	Tyr	Thr	-		
l le 305		, Asn	Val	Ala	Arg 310		Arg	Thr	Tyr	Glu 315		Ala	Val	Ala	Leu 320			
Asp	Thr	Glu	lle	Pro 325		Glu	Leu	Pro	Tyr 330		Asp	Tyr	Phe	Glu 335		•		
Phe	Gly	Pro	Asp 340	Phe	Lys	Leu	His	11e 345	Ser	Pro	Ser	Asn	Met 350		Asn			
GIn	Asn	Thr 355		Glu	Tyr	Leu	Glu 360	Lys	lle	Lys	Gln	Arg 365		Phe	Glu			
Asn	Leu 370	Arg	Met	Leu	Pro	His 375	Ala	Pro	Gly	Val	GIn 380	Met	Gln	Ala	He			
Pro 385	Glu	Asp	Ala	He	Pro 390	Glu	Glu	Ser	Gly	Авр 395	Glu	Asp	Glu	Asp	Asp 400			
Pro	Asp ·	Lys	Arg	lle 405	Ser	lle	Cys	Ser	Ser 410	Asp	Lys	Arg	lle	Ala 415	Cys			
Glu	Glu	Glu	Phe 420	Ser	Asp	Ser	Glu	Glu 42 5	Glu.	Gly	Glu	Gly	Gly 430	Arg	Lys			
Asn	Ser	Ser 435	Asn	Phe	Lys	Lys	A I a 440	Lys	Arg	Val	Lys	Thr 445	Glu	Asp	Glu			
Lys	Glu 450	Lys	Asp	Pro	Glu	G1u 455	Lys	Lys	Glu	Val	Thr 460	Glu	Glu	Glu	Lys			
465		Glu	Glu	Lys	Pro 470	Glu	Ala	Lys		Va I 475		Glu	Glu	Val	Lys 480			
Leu	Ala																	
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<400 atg			acg (cag	ggc	acc	CEE :	agg :	aaa .	gtc	tgt '	tac	tac	tac	gac		48	
Met 1			Thr					Arg									_	
ggg (gat	gtt	gga a	aat	tac	tat	tat	gga	caa	ggc	cac	cca .	atg	aag	cct		96	

Gly Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro 20 25 30 144 cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg Arg Lys Met Glu lle Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met 50 55 60 192 acc aag tac cac agc gat gac tac att aaa tto ttg cgc toc atc cgt Thr Lys Tyr His Ser Asp Asp Tyr IIe Lys Phe Leu Arg Ser IIe Arg 240 288 90 336 384 432 480 528

cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt Pro Asp Asn Met Ser Glu Tyr Ser Lys Gin Met Gin Arg Phe Asn Val ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu 100 105 110 tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln 115 120 125 acg gac atc gct gtg aat tgg gct ggg ggc ctg aag ctt gca aag aag Thr Asp IIe Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys 130 135 140 too gag goa tot ggo tto tgt tac gtc aat gat atc gtc ttg goc atc Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp 165 170 175 att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg lle His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg 576 gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga act Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr 195 200 205 624 ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt Gly Asp Leu Arg Asp lle Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val 210 215 220 672 aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att Asn Tyr Pro Leu Arg Asp Gly IIe Asp Asp Gly Ser Tyr Glu Ala IIe 720 ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 768 250 gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt Val Val Leu Gin Cys Giy Ser Asp Ser Leu Ser Giy Asp Arg Leu Giy 260 265 270 816 tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc Cys Phe Asn Leu Thr lie Lys Gly His Ala Lys Cys Val Glu Phe Val 864 aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr 290 295 300 att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg lle Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu 305 310 320

													0959	Я		
					Asn					Asn		tac	ttt	gaa	tac Tyr	1008
ttt Phe	gga Gly	cca Pro	gat Asp 340	Phe	aag Lys	ctc Leu	cac His	atc Ile 345	Ser	cct Pro	tcc Ser	aat Asn	atg Met 350	act Thr	aac Asn	1056
cag Gin	aac Asn	acg Thr 355	Asn	gag Glu	tac Tyr	ctg Leu	gag Glu 360	aag Lys	atc lle	aaa Lys	cag Gin	cga Arg 365	ctg Leu	ttt Phe	gag Glu	1104
aac Asn	ctt Leu 370	aga Arg	atg Met	ctg Leu	ccg Pro	cac His 375	gca Ala	cct Pro	ggg G y	gtc Val	caa Gin 380	atg Met	cag Gin	gcg Ala	att He	1152
cct Pro 385	Glu	gac Asp	gcc Ala	atc ile	cct Pro 390	gag Glu	gag Glu	agt Ser	ggc Gly	gat Asp 395	gag Glu	gac Asp	gaa Glu	gac Asp	gac Asp 400	1200
												cga Arg				1248
gag Glu	gaa Glu	gag Glu	ttc Phe 420	tcc Ser	gat Asp	tct Ser	gaa Glu	gag Glu 425	gag Glu	gga Gly	gag Glu	ggg Gly	ggc Gly 430	cgc Arg	aag Lys	1296
aac Asn	tct Ser	tcc Ser 435	aac Asn	ttc Phe	aaa Lys	Lys	gcc Ala 440	aag Lys	aga Arg	gtc Val	aaa Lys	aca Thr 445	gag Glu	gat Asp	gaa Glu	1344
					Glu							gaa Glu				1392
acc Thr 465	aag Lys	gag Glu	gag Glu	Lys	cca Pro 470	gaa Glu	gcc Ala	aaa Lys	Gly	gtc Val 475	aag Lys	gag Glu	gag Glu	gtc Val	aag Lys 480	1440
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PRT Artificial

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Dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

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His Arg IIe Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr 35 40 45

Arg Lys Met Glu lle Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met 50 60

Thr Lys Tyr His Ser Asp Asp Tyr IIe Lys Phe Leu Arg Ser IIe Arg 65 75 80

NOEGO			

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val 85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu 100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln 115 120 125

Thr Asp IIe Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp IIe Val Leu Ala IIe 145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr lle Asp lle Asp 165 170 175

lle His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg 180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr 195 200 205

Gly Asp Leu Arg Asp IIe Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Vai 210 215 220

Asn Tyr Pro Leu Arg Asp Gly IIe Asp Asp Glu Ser Tyr Glu Ala IIe 225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 245 250 255

Val Val Leu Gin Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly 260 265 270

Cys Phe Asn Leu Thr IIe Lys Gly His Ala Lys Cys Val Glu Phe Val 275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr 290 295 300

lie Arg Asn Val Ala Arg Cys Arg Thr Tyr Giu Thr Ala Val Ala Leu 305 310 315 320

Asp Thr Glu lle Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr 325 330 335

Phe Gly Pro Asp Phe Lys Leu His IIe Ser Pro Ser Asn Met Thr Asn 340 345 350

Gin Asn Thr Asn Giu Tyr Leu Giu Lys IIe Lys Gin Arg Leu Phe Giu 355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gin Met Gin Ala Ile 370 375 380

Pro	o Ası	p Ly:	s Arg	11e 405		lle	Cys	Ser	Ser 410) Lys	Arı	g IIo	41:	a Cys	
Gli	ı Glı	G L	. Phe 420		Asp	Ser	Glu	Glu 425		Gly	/ GIL	Gly	430		g Lys	
Ası	n Ser	- Ser 435		Phe	Lys	Lys	Ala 440		Arg	Val	Lys	Thr 445		ı Ast	Glu	
Lys	450		s Asp	Pro	Glu	Glu 455		Lys	Glu	Val	Thr 460		ı Git	ı Glu	ı Lys	
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Leu	ıAla	1														
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atg		cag		cag Gin 5												48
				aat Asn												96
cac His	cga Arg	atc Ile 35	cgc Arg	atg Met	act Thr	cat His	aat Asn 40	ttg Leu	ctg Leu	ctc Leu	aac Asn	tat Tyr 45	ggt Gly	ctc Leu	tac Tyr	144
				atc Ile	Tyr											192
				agc Ser					Lys							240
cca Pro	gat Asp	aac Asn	atg Met	tog Ser 85	gag Glu	tac Tyr	agc Ser	aag Lys	cag Gin 90	atg Met	cag Gin	aga Arg	ttc Phe	aac Asn 95	gtt Val	288
				cca Pro			Asp									336
tct Ser	act Thr	ggt Gly 115	ggt Gly	tct Ser	gtg Val	Ala	agt Ser 120	gct Ala	gtg Val	aaa Lys	Leu	aat Asn 125	aag Lys	cag Gin	cag Gln	384
acg Thr	gac Asp	atc lle	gct Ala	gtg : Val :	aat Asn	tgg Trp	gct Ala	ggg Gly	ggc Gly	ctg Leu	cac His	His	gca Ala (31)	aag Lys	aag Lys	432

Pro Glu Asp Ala IIe Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp 385 Asp 400

		_									• • •	_				
	r Glu					e Cys					110				c atc a lle 160	480
					Tyr					Leu					t gat e Asp	528
ati	t cad e His	c cat s His	t ggt s Gly 180	/ Asp	ggo Gly	gtg Val	gaa Glu	gag Glu 185	ı Ala	tto Phe	tac Tyr	acc Thr	ace Thr 190	. Ast	c cgg o Arg	576
			· Val					Tyr					Pro		act Thr	624
		Leu					Āla					Tyr			gtt Val	672
	Tyr					Gly					Ser				att lle 240	720
					Ser					Met					gcg	768
			cag Gin 260											Leu		816
tgc Cys	ttc Phe	aat Asn 275	cta Leu	act Thr	atc lle	aaa Lys	gga Gly 280	cac His	gcc Ala	aag Lys	tgt Cys	gtg Val 285	gaa Glu	ttt Phe	gtc Val	864
		Phe	aac Asn													912
	Arg		gtt Val													960
			atc Ile													1008
			gat Asp 340													1056
cag Gin	aac Asn	acg Thr 355	aat Asn	gag Glu	tac Tyr	Leu	gag Glu 360	aag Lys	atc He	aaa Lys	cag Gin	cga Arg 365	ctg Leu	ttt Phe	gag Glu	1104
			atg Met													1152
cct Pro 385	gag Glu	gac Asp	gcc Ala	atc Ile	cct Pro 390	gag Glu	gag Glu	agt Ser	Gly	gat Asp 395	gag Glu	gac Asp	gaa Glu	gac Asp	gac Asp 400	1200
			cgc Arg					Ser								1248
gag Glu	gaa Glu	gag Glu	ttc Phe 420	tcc Ser	gat Asp	tct Ser	Glu	gag Glu 425	gag Glu	gga Gly	gag Glu	ggg Gly	ggc Gly 430	cgc Arg	aag Lys	1296
aac	tct	tcc	aac	ttc	aaa	aaa	gcc	aag	aga	gtc	aaa		gag (32)	gat	gaa	1344

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu 435 440 445

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ttg gcc tga 1449 Leu Ala

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⟨213⟩ Artificial

<220>
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His Arg IIe Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr 35 40 45

Arg Lys Met Glu lle Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met 50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr IIe Lys Phe Leu Arg Ser IIe Arg 65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Vai 85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu 100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln 115 120 125

Thr Asp IIe Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile 145 150 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr lle Asp 11e Asp 175 175

lle His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg 180 185 190

Val Met Thr Val Ser Phe Leu Lys Tyr Gly Glu Tyr Phe Pro Gly Thr

Gly Asp Leu Arg Asp lie Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val 210 215 220

Asn Tyr Pro Leu Arg Asp Gly IIe Asp Asp Glu Ser Tyr Glu Ala IIe 225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 245 250 255

Val Val Leu Gin Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly 260 265 270

Cys Phe Asn Leu Thr IIe Lys Gly His Ala Lys Cys Val Glu Phe Val 275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Giy Giy Giy Tyr Thr 290 295 300

lle Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu 305 310 315 320

Asp Thr Glu lie Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr 325 330 335

Phe Gly Pro Asp Phe Lys Leu His IIe Ser Pro Ser Asn Met Thr Asn 340 345

Gin Asn Thr Asn Giu Tyr Leu Giu Lys IIe Lys Gin Arg Leu Phe Giu 355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gin Met Gin Ala IIe 370 375 380

Pro Glu Asp Ala IIe Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp 385 390 395 400

Pro Asp Lys Arg IIe Ser IIe Cys Ser Ser Asp Lys Arg IIe Ala Cys 405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys 420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Vai Lys Thr Glu Asp Glu 435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Vai Thr Glu Glu Glu Lys 450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys 465 470 475 480

Leu Ala

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															acc Thr	96
cat His	agc Ser	ctg Leu 35	gtc Val	ctg Leu	cat His	tac Tyr	ggt Gly 40	ctc Leu	tat Tyr	aag Lys	aag Lys	atg Met 45	atc	gtc Val	ttc Phe	144
aag Lys	cca Pro 50	tac Tyr	cag Gin	gcc	tcc Ser	caa Gin 55	cat His	gac Asp	atg Met	tgc Cys	cgc Arg 60	ttc Phe	cac His	tcc Ser	gag Glu	192
gac Asp 65	tac Tyr	att	gac Asp	ttc Phe	ctg Leu 70	cag Gin	aga Arg	gtc Val	agc Ser	ccc Pro 75	acc Thr	aat Asn	atg Met	caa Gin	ggc Gly 80	240
ttc Phe	acc Thr	aag Lys	agt Ser	ctt Leu 85	aat Asn	gcc Ala	ttc Phe	aac Asn	gta Val 90	ggc Gly	gat Asp	gac Asp	tgc Cys	cca Pro 95	gtg Val	288
					gag Glu									Ser		336
			Thr		ctg Leu											384
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	Tyr				att e 150											480
cac His	cct Pro	cgg Arg	gtg Val	ctc Leu 165	tac Tyr	att	gac Asp	att He	gac Asp 170	atc Ile	cac His	cat His	ggt Gly	gac Asp 175	ggg Gly	528
gtt Val	caa Gin	gaa Glu	gct Ala 180	ttc Phe	tac Tyr	ctc Leu	act Thr	gac Asp 185	cgg Arg	gtc Val	atg M et	acg Thr	gtg Val 190	tcc Ser	ttc Phe	576
					tac Tyr											624
gtc Val	ggg Gly 210	gca Ala	gag Glu	agt Ser	ggc Gly	cgc Arg 215	tac Tyr	tac Tyr	tgt Cys	ctg Leu	aac Asn 220	gtg Val	ccc Pro	ctg Leu	cgg Arg	672
gat Asp 225	ggc Gly	att lle	gat Asp	gac Asp	cag Gin 230	agt Ser	tac Tyr	aag Lys	cac His	ctt Leu 235	ttc Phe	cag Gin	ccg Pro	gtt Val	atc Ile 240	720
					ttc Phe											768

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					r Le					Leu					n Lei	c agc u Ser	816
				y Hi					GIL					Phe		t atc n lle	864
			Lei					Gly					Arg			t gcc i Ala	912
A							ı Thr					Glu				agt Ser 320	960
g	ag	gag Glu	ct1 Lei	t cc	tato Tyr 325	- Ser	gaa Glu	tac Tyr	ttc Phe	gag Glu 330	Tyr	ttt Phe	gcc	Pro	a gad o Asp 335	ttc Phe	1008
) Asp					ile					Ser	cgc Arg	1056
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								Gin					Pro			ctc Leu	1152
L							gat Asp					Glu					1200
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ga As	ac sp	cat His	gac Asp	aat Asn 420	Asp	aag Lys	gaa Glu	agc Ser	gat Asp 425	gtg Val	gag Glu	att lle	taa				1287
\(\frac{1}{2}\)	210 211 212 213	> 4 > F	6 128 PRT Iomo	sap	iens												
	100) et /		6 Lys	Thr	Val 5	Ala	Tyr	Phe	Tyr	Asp 10	Pro	Asp	Val	Gly	Asn 15	Phe	
Hi	s	Tyr	Gly	Ala 20	Gly	His	Pro	Met	Lys 25	Pro	His	Arg	Leu	Ala 30	Leu	Thr	
Hi	s	Ser	Leu 35	Val	Leu	His	Tyr	G y 40	Leu	Tyr	Lys	Lys	Met 45	lle	Val	Phe	
Ly		Pro 50	Tyr	Gln	Ala	Ser	GIn 55	His	Asp	Met	Cys	Arg 60	Phe	His	Ser	Glu	
As 65		Гуr	lle	Asp	Phe	Leu 70	Gln	Arg	Val	Ser	Pro 75	Thr	Asn	Met	GIn	Gly 80	
Ph	e 7	ſhr	Lys	Ser	Leu 85	Asn	Ala	Phe		Va I 90	Gly	Asp	Asp	Cys	Pro 95	Val	

Phe	. Pro	Gly	/ Leu 100		Glu	Phe	Cys	Ser 105		Tyr	Thr	Gly	0959 Ala 110	Ser	· Leı
Gln	Gly	Ala 115	Thr	GIn	Leu	Asn	Asn 120		ile	Cys	Asp	11e 125		lle	Asn
Trp	130		Gly	Leu	His	His 135		Lys	Lys	Phe	Glu 140		Ser	Gly	Phe
Cys 145		Val	Asn	Asp	11e 150	Val	lle	Gly	lle	Leu 155		Leu	Leu	Lys	Tyr 160
His	Pro	Arg	Va I	Leu 165		lle	Asp	lle	Asp 170	He	His	His	Gly	Asp 175	
Val	GIn	Glu	Ala 180		Tyr	Leu	Thr	Asp 185	Arg	Val	Met	Thr	Va I 190		Phe
His	Lys	Tyr 195	Gly	Asn	Tyr	Phe	Phe 200	Pro	Gly	Thr	Gly	Asp 205	Met	Tyr	Glu
Val	Gly 210		Giu	Ser	Gly	Arg 215	Tyr	Tyr	Cys	Leu	Asn 220	Val	Pro	Leu	Arg
Asp 225		lle	Asp	Asp	GIn 230	Ser	Tyr	Lys	His	Leu 235	Phe	Gln	Pro	Val	11e 240
Asn	GIn	Val	Val	Asp 245	Phe	Tyr	Gln	Pro	Thr 250	Cys	lle	Val	Leu	GIn 255	Cys
Gly	Ala	Asp	Ser 260	Leu	Gly	Cys	Asp	Arg 265	Leu	Gly	Cys	Phe	Asn 270	Leu	Ser
He	Arg	Gly 275	His	Gly	Glu	Cys	Va I 280	Glu	Tyr	Val	Lys	Ser 285	Phe	Asn	lle
Pro	Lец 290	Leu	Val	Leu	Gly	Gly 295	Gly	Gly	Tyr	Thr	Va I 300	Arg	Asn	Val	Ala
Arg 305	Cys	Trp	Thr	Tyr	Glu 310	Thr	Ser	Leu	Leu	Va I 315	Glu	Glu	Ala	He.	Ser 320
Glu	Glu	Leu	Pro	Tyr 325	Ser	Glu	Tyr	Phe	Glu 330	Tyr	Phe	Ala	Pro	Asp 335	Phe
Thr	Leu	His	Pro 340	Asp	Val	Ser	Thr	Arg 345	He	Glu	Asn	Gin	Asn 350	Ser	Arg

Leu Asn His Ala Pro Ser Val Gln IIe His Asp Val Pro Ala Asp Leu 370

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro 385

Gin Tyr Leu Asp Gin IIe Leu Gin Thr IIe Phe Giu Asn Leu Lys Met 355 360 365

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly $405 \hspace{1cm} 410 \hspace{1cm} 415$

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu IIe 420 425

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											cgc Arg				acc Thr	96
											aag Lys					144
											cgc Arg 60					192
											acc Thr					240
											gat Asp					288
ttt Phe	ccc Pro	ggg Gly	ctc Leu 100	ttt Phe	gag Glu	ttc Phe	tgc Cys	tog Ser 105	cgt Arg	tac Tyr	aca Thr	ggc Gly	gca Ala 110	tct Ser	ctg Leu	336
											gat Asp					384
											gag Glu 140					432
											gag Glu					480
											cac His					528
											atg Met					576
											ggt Gly					624
gtc Val	ggg Gly	gca Ala	gag Glu	agt Ser	ggc Gly	cgc Arg	tac Tyr	tac Tyr	tgt Cys	ctg Leu	aac Asn	gtg Val	ccc Pro	ctg Leu	cgg Arg	672

	Ġly					Ser					Phe				atc lle 240	720
aac Asr	cag Glr	gta Val	gtg Val	gac Asp 245	Phe	tac Tyr	Gin	cco Pro	acg Thr 250	Cys	att	gtg Val	cto Leu	Gln 255	tgt Cys	768
			tct Ser 260	Leu					Leu					Leu	agc Ser	816
			cat His					Glu					Phe			864
		Leu	gtg Val									Arg				912
	Cys		aca Thr													960
			ccc Pro													1008
			cca Pro 340													1056
			gac Asp													1104
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His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met IIe Val Phe 35 40 45

- Lys Pro Tyr Gin Ala Ser Gin His Asp Met Cys Arg Phe His Ser Glu 50 60
- Asp Tyr lie Asp Phe Leu Gin Arg Val Ser Pro Thr Asn Met Gin Giy 65 75 80
- Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val 85 90 95
- Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu 100 105 110
- Gin Gly Ala Thr Gin Leu Asn Asn Lys IIe Cys Asp IIe Ala IIe Asn 115 120 125
- Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys Phe Glu Ala Ser Gly Phe 130 135 140
- Cys Tyr Val Asn Asp lie Val lie Gly lie Leu Glu Leu Leu Lys Tyr 145 150 155 160
- His Pro Arg Val Leu Tyr lle Asp lle Asp lle His His Gly Asp Gly 165 170 175
- Val Gin Giu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe 180 185 190
- His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu 195 200 205
- Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg 210 215 220
- Asp Gly IIe Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val IIe 225 230 235 240
- Asn Gin Val Val Asp Phe Tyr Gin Pro Thr Cys lie Val Leu Gin Cys 245 250 255
- Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser 260 265 270
- lle Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile 275 280 285
- Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val Ala 290 295 300
- Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala IIe Ser 305 310 315 320
- Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe 325 330 335
- Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg

Gin Tyr Leu Asp Gin IIe Leu Gin Thr IIe Phe Giu Asn Leu Lys Met 355 360 365

Leu Asn His Ala Pro Ser Val Gln IIe His Asp Val Pro Ala Asp Leu 370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro 385 390 395

Giu Giu Asn Tyr Ser Arg Pro Giu Ala Pro Asn Giu Phe Tyr Asp Giy 405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu IIe 420 425

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cac tac His Tyr	gga gct Gly Ala 20	gga cad Gly His	cct atg Pro Met	aag co Lys Pro 25	cat cgo His Arg	c ctg gca g Leu Ala 30	ttg ac Leu Th	c 96 r
cat agc His Ser	ctg gtc Leu Val 35	ctg cat Leu His	tac ggt Tyr Gly 40	ctc ta	t aag aag Lys Lys	atg atc Met Ile 45	gtc tto Val Pho	c 144 e
aag cca Lys Pro 50	tac cag Tyr Gin	gcc tcc Ala Ser	caa cat Gin His 55	gac atı Asp Met	tgc cgc Cys Arg 60	ttc cac Phe His	tcc gar Ser Gli	g 192 J
						aat atg Asn Met		
						gac tgc Asp Cys		
ttt ccc Phe Pro	ggg ctc Gly Leu 100	ttt gag Phe Glu	ttc tgc Phe Cys	tog ogt Ser Arg 105	tac aca Tyr Thr	ggc gca Gly Ala 110	tct ctg Ser Leu	336
Gin Gly	gca acc Ala Thr 115	cag ctg Gin Leu	aac aac Asn Asn 120	Lys IIe	tgt gat Cys Asp	att gcc lle Ala 125	att aad lle Asr	384
tgg gct Trp Ala 130	ggt ggt Gly Gly	ctg cac Leu His	cat gcc His Ala 135	aag aag Lys Lys	ttt gag Phe Glu 140	gcc tct Ala Ser	ggo tto Gly Phe	432
tgc tat (Cys Tyr 145	gtc aac Val Asn	gac att Asp lle 150	gtg att Val lle	ggc atc Gly lle	ctg gag Leu Glu 155	ctg ctc Leu Leu	aag tad Lys Tyr 160	•

													0959	8		
cac His	cct Pro	cgg Arg	gtg Val	ctc Leu 165	tac Tyr	att	gac Asp	att	gac Asp 170	atc le	cac His	cat	ggt	gac	ggg G y	528
gtt Vai	caa Gin	gaa Glu	gct Ala 180	Phe	tac Tyr	ctc Leu	act Thr	gac Asp 185	Arg	gtc Val	atg Met	acg Thr	gtg Val 190	Ser	ttc Phe	576
			Gly									gac Asp 205				624
gtc Val	ggg Gly 210	Ala	gag Glu	agt Ser	ggc Gly	cgc Arg 215	tac Tyr	tac Tyr	tgt Cys	ctg Leu	aac Asn 220	gtg Vai	ccc Pro	ctg Leu	cgg Arg	672
gat Asp 225	Gly	att lle	gat Asp	gac Asp	cag Gin 230	agt Ser	tac Tyr	aag Lys	cac His	ctt Leu 235	ttc Phe	cag Gin	ccg Pro	gtt Val	atc lle 240	720
aac Asn	cag Gin	gta Val	gtg Val	gac Asp 245	ttc Phe	tac Tyr	caa Gin	ccc Pro	acg Thr 250	tgc Cys	att He	gtg Val	ctc Leu	cag Gin 255	tgt Cys	768
gga Gly	gct Ala	gac Asp	tct Ser 260	ctg Leu	ggc Gly	tgt Cys	gat Asp	cga Arg 265	ttg Leu	ggc Gly	tgc Cys	ttt Phe	aac Asn 270	ctc Leu	agc Ser	816
atc Ile	cga Arg	ggg Gly 275	cat His	ggg Gly	gaa Glu	tgc Cys	gtt Val 280	gaa Glu	tat Tyr	gtc Val	aag Lys	agc Ser 285	ttc Phe	aat Asn	atc lle	864
cct Pro	cta Leu 290	ctc Leu	gtg Val	ctg Leu	ggt Gly	ggt Gly 295	ggt Gly	ggt Gly	tat Tyr	act Thr	gtc Val 300	cga Arg	aat Asn	gtt Val	gcc Ala	912
cgc Arg 305	tgc Cys	tgg Trp	aca Thr	tat Tyr	gag Glu 310	aca Thr	tcg Ser	ctg Leu	ctg Leu	gta Val 315	gaa Glu	gag Glu	gcc Ala	att	agt Ser 320	960
gag Glu	gag Glu	ctt Leu	ccc Pro	tat Tyr 325	agt Ser	gaa Glu	tac Tyr	ttc Phe	gag Glu 330	tac Tyr	ttt Phe	gcc Ala	cca Pro	gac Asp 335	ttc Phe	1008
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cag Gin	tat Tyr	ctg Leu 355	gac Asp	cag Gin	atc lle	ctc Leu	cag Gin 360	aca Thr	atc ile	ttt Phe	gaa Glu	aac Asn 365	ctg Leu	aag Lys	atg Met	1104
ctg Leu	aac Asn 370	cat His	gca Ala	cct Pro	agt Ser	gtc Val 375	cag Gin	att ile	cat His	gac Asp	gtg Val 380	cct Pro	gca Ala	gac Asp	ctc Leu	1152
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			Tyr									ttc Phe				1248
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(223) Dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

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His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe 35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu 50 60

Asp Tyr IIe Asp Phe Leu Gin Arg Val Ser Pro Thr Asn Met Gin Gly 65 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val 85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu 100 105 110

Gin Gly Ala Thr Gin Leu Asn Asn Lys IIe Cys Asp IIe Ala IIe Asn 115 120 125

Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe 130 . 135 140

Cys Tyr Val Asn Asp IIe Val IIe Gly IIe Leu Glu Leu Leu Lys Tyr 145 150 160

His Pro Arg Val Leu Tyr lle Asp lle Asp lle His His Gly Asp Gly 165 170 175

Val Gin Giu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe 180 185 190

Leu Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu 195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg 210 215 220

Asp Gly IIe Asp Asp Gin Ser Tyr Lys His Leu Phe Gin Pro Val IIe 225 230 235 240

Asn Gin Val Val Asp Phe Tyr Gin Pro Thr Cys lie Val Leu Gin Cys 245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser 260 265 270

lle Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile 275 280 285

Pro	290		ı Val	Leu	ı Giy	295		Gly	lyr	Ihr	300		, AST	val	Ala	
Arg 305		Trp	Thr	Tyr	Glu 310		Ser	Leu	Leu	Va l 315		Glu	Ala	lle	Ser 320	
Glu	Glu	ı Leu	ı Pro	Tyr 325		Glu	Tyr	Phe	Glu 330		Phe	Ala	Pro	Asp 335	Phe	
Thr	Leu	ı His	Pro 340		Val	Ser	Thr	Arg 345		Glu	Asn	Gin	Asn 350		Arg	
Gin	Tyr	Leu 355		GIn	lle	Leu	Gin 360		ile	Phe	Glu	Asn 365		Lys	Met	
Leu	Asn 370		Ala	Pro	Ser	Val 375		lle	His	Asp	Va I 380		Ala	Asp	Leu	
Leu 385		Tyr	Asp	Arg	Thr 390		Glu	Ala	Asp	Ala 395		Glu	Arg	Gly	Pro 400	
Glu	Glu	Asn	Tyr	Ser 405	Arg	Pro	Glu	Ala	Pro 410	Asn	Glu	Phe	Tyr	Asp 415	Gly	
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					acc Thr	Thr										144
					tca Ser											192
	Asn				tac Tyr 70											240
			Leu		ctg Leu			Gln								288
					aag Lys											336

			Glu					Arg					Gly		gtc Val	384
		Thr					Gin					Thr			act Thr	432
GCE Pro 145	Thr	ago Ser	aaa Lys	att	tca Ser 150	Val	gag Glu	agc Ser	att	cca Pro 155	Ser	cta Leu	cgg Arg	ggo	tct Ser 160	480
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			Gly					gca Ala								624
gaa Glu	ggc Gly 210	Lys	agt Ser	gga Gly	cat His	atc lle 215	ttg Leu	tca Ser	tat Tyr	gat Asp	aat Asn 220	He	aag Lys	aat Asn	gcc Ala	672
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ata He	cga Arg	gca Ala	ttt Phe	gaa Glu 325	ggt Gly	gcc Ala	att	acc Thr	aaa Lys 330	gga Gly	aaa Lys	cca Pro	tat T y r	gat Asp 335	ggc Gly	1008
								cgt Arg 345								1056
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				Asn				tct Ser	Ala							1200
								cta Leu								1248

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ga: Gli	a at	t gta e Va	g cca I Pro 420	o Gil	g aac u Asr	ata ille	aaa Lys	gtg Val	Val	a gaa Glu	a cgg ı Arg	gga	a aaa / Lys 430	Tyr	gag Glu
ga [*] Ası	t gte o Va	g aaa I Lys 435	s Ala	a ggo a Gly	gag Glu	acc Thr	gtg Val 440	Are	t too Ser	cgs Ars	g cac g His	acg Thr 445	Ser	gtg Val	gta Val
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	Glr					lle					Ser				acc Thr 480
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lle	Pro	Ser 35	Ser	Lys	Thr	Thr	Val 40	Ala	Ser	Glu	Lys	Pro 45	Ser	Phe	lle
Met	Gly 50	Gly	Ser	lle	Ser	GIn 55	Gly	Thr	Pro	Gly	Thr 60	Tyr	Leu	Thr	Ser
His 65	Asn	Gln	Ala	Ser	Tyr 70	Thr	Gln	Glu	Thr	Pro 75	Lys	Pro	Ser	Val	Gly 80
Ser	lle	Ser	Leu	Gly 85	Leu	Pro	Arg	Gin	GIn 90	Glu	Ser	Ala	Lys	Ser 95	Ala
Thr	Leu	Pro	Tyr 100	He	Lys	GIn	Glu	Glu 105	Phe	Ser	Pro	Arg	Ser 110	Gin	Asn
Ser	Gin	Pro 115	Glu	Gly	Leu	Leu	Va I 120	Arg	Ala	Gln	His	Glu 125	Gly	Val	Val
Arg	Gly 130	Thr	Ala	Gly	Ala	lle 135	Gln	G lu	Gly	Ser	I le 140	Thr	Arg	Gly	Thr
Pro 145	Thr	Ser	Lys	Пe	Ser 150	Val	Glu	Ser	He	Pro 155	Ser	Leu	Arg	Gly	Ser 160
lle	Thr	GIn	Gly	Thr 165	Pro	Ala	Leu	Pro	GIn 170	Thr	Gly	He	Pro	Thr 175	Glu
Ala	Leu	Val	Lys 180	Gly	Ser	lle	Ser	Arg 185	Met	Pro	ile	Glu	Asp 190	Ser	Ser

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- Glu Gly Lys Ser Gly His IIe Leu Ser Tyr Asp Asn IIe Lys Asn Ala 210 215 220
- Arg Glu Gly Thr Arg Ser Pro Arg Thr Ala His Glu IIe Ser Leu Lys 225 230 235 240
- Arg Ser Tyr Glu Ser Val Glu Gly Asn IIe Lys Gln Gly Met Ser Met 245 250 255
- Arg Glu Ser Pro Val Ser Ala Pro Leu Glu Gly Leu lle Cys Arg Ala 260 265 270
- Leu Pro Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu 275 280 285
- Ser Gly Ser lie Met Gin Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe 290 295 300
- Glu Asp Gly Leu Lys Tyr Pro Lys Gin IIe Lys Arg Glu Ser Pro Pro 305 310 315 320
- lle Arg Ala Phe Glu Gly Ala lle Thr Lys Gly Lys Pro Tyr Asp Gly 325 330 335
- lle Thr Thr lle Lys Glu Met Gly Arg Ser lle His Glu lle Pro Arg 340 345 350
- Gin Asp IIe Leu Thr Gin Glu Ser Arg Lys Thr Pro Glu Val Val Gin 355 360 365
- Ser Thr Arg Pro IIe IIe Glu Gly Ser IIe Ser Gln Gly Thr Pro IIe 370 375 380
- Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala lie Lys His Asn Val Lys 385 390 400
- Ser Leu lie Thr Gly Pro Ser Lys Leu Ser Arg Gly Met Pro Pro Leu 405 410 415
- Glu lie Val Pro Glu Asn lie Lys Val Val Glu Arg Gly Lys Tyr Glu 420 425 430
- Asp Val Lys Ala Gly Glu Thr Val Arg Ser Arg His Thr Ser Val Val 435 440 445
- Ser Ser Gly Pro Ser Val Leu Arg Ser Thr Leu His Glu Ala Pro Lys 450 455 460
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      5'-flanking region of Human interleukin-2 (IL-2) gene
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 agatatataa toattttaaa ttaaaatago gttaaacagt acctcaagot caataagcat
                                                                        120
tttaagtatt ctaatcttag tatttctcta gctgacatgt aagaagcaat ctatcttatt
                                                                        180
                                                                        240
gtatgcaatt agctcattgt gtggataaaa aggtaaaacc attctgaaac aggaaaccaa
                                                                        300
tacacttcct gtttaatcaa caaatctaaa catttattct tttcatctgt ttactcttgc
tcttgtccac cacaatatgc tattcacatg ttcagtgtag ttttaggaca aagaaaattt
                                                                        360
totgagttac ttttgtatcc ccacccctt aaagaaagga ggaaaaactg tttcatacag
                                                                       420
aaggogttaa ttgcatgaat tagagctatc acctaagtgt gggctaatgt aacaaagagg
                                                                        480
                                                                        540
gatttcacct acatccattc agtcagtctt tgggggttta aagaaattcc aaagagtcat
cagaagagga aaaatgaagg taatgttttt tcagacaggt aaagtctttg aaaatatgtg
                                                                        600
taatatgtaa aacattttga cacccccata atatttttcc agaattaaca gtataaattg
                                                                        660
catctcttgt tcaagagttc cctatcactc tctttaatca ctactcacag taacctcaac
                                                                        720
                                                                        731
tcctgccaca a
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       24
(211)
       527
(212)
       DNA
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(221)
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5'-flanking region of Human interleukin-2 (IL-2) gene
(222>
〈223〉
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cccttcgcta gctgctcttg tccaccacaa tatgctattc acatgttcag tgtagtttta
                                                                        120
                                                                       180
ggacaaagaa aattttctga gttacttttg tatccccacc cccttaaaga aaggaggaaa
aactgtttca tacagaaggc gttaattgca tgaattagag ctatcaccta agtgtgggct
                                                                       240
                                                                       300
aatgtaacaa agagggattt cacctacatc cattcagtca gtctttgggg gtttaaagaa
attocaaaga gtoatoagaa gaggaaaaat gaaggtaatg ttttttoaga caggtaaagt
                                                                       360
ctttgaaaat atgtgtaata tgtaaaacat tttgacaccc ccataatatt tttccagaat
                                                                       420
taacagtata aattgcatct cttgttcaag agttccctat cactctcttt aatcactact
                                                                       480
                                                                       527
cacagtaacc tcaactcctg ccacaagctt cgaagggcga attcgtt
⟨210⟩
      25
      900
(211)
      DNA
<213>
      Homo sapiens
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ctggctccca cctcagtttc ccgcctccaa ggcagcatgg cgggcaagaa gttgaggcca	120
ctgtccctgg gtgttcctac ccccacaccc tcaccccaag acagcctgtt actgcggcgc	180
caacagccac ggtcgcctac atctgataag acttatctgc tgccccaggg caggccggag	240
ctggcgtaag ccccagtggg gcgctaagtg agtgtgcccc tgcctcccgc cagcactggc	300
ctggcctgca ggcttagcct gggtcatcaa ggtatcccac aggctctagt tcaaatccag	360
cagaacctct ctgagcctca ctcttctcac ctgcaaaatg ggtacagcca catcccttct	420
ctccctgcag ccaggaagac gcacatacac aggagtctag cccacaccgg ccccgcacaa	480
attaaggget ttactetetg aaaageecag tgaagteatg aaaceatate tgetatttte	540
atttatcttg gtttcagcct attttgcttg tctggacact acagtccacg ggagcctagg	600
togagogagg tocaagaato cocagggtgg goagggaggg tggaagaggg cotocagtgo	660
ccaagaggtg ccccacaagc atgggacccg ccccctcccc tggactgccc cacccactgg	720
ggcaccagcc actccctggg gaggagggag gagggagaag ggagggaggg agggagggag	780
gaagggagcc tcaaaggcca aggccagcca ggacaccccc tgggatcaca ctgagcttgc	840
cacatcccca aggoggooga accotccgca accaccaaag cttataaggg cgaattcgtt	900
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⟨210⟩ 26	
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aagagaggac attgaagaag agtotcaaac ttaggootga oggagaagac gogoggocag	120
gacaccccac ccccgccctc gtctccccca aagcctgatc tggccccact gattccctta	180
totgcccact cccagctgcc tocttgctgg ctgaactgtc gccgcagact tctgagcctg	240
cgccccctcc acggggatgg gggagggaat ggggtgaggc ctggcctcac agcctcgggg	300
tttccagctc ttgctggagg cagggctctg gggcgcccta ctcctcaccc ttggcttctc	360
ttcctgagcg ctctgtgctc tccagaaatg aagaaatggg gtgagtccag cggccaaacc	420
cttgtcttag ctcttagaca tgcctcgagc ctgccattcc ctgtgaggac agatttccct	480
atgttgcgac cgctgcttct aataataata atgatgatga taattcccat ttacagagca	540
caccatttat ggtgtgccag caggccctgt gctgagtggt tcctacccac gtggggggct	600
aggactitac ccgtittcca gatgaagaaa ctgaggctca gagggcgcta gcataagggc	660
(210) 27 (211) 32	
(212) DNA	

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 〈223〉
        PCR primer for amplifying the 5'-flanking region of Human interleukin-2
         (IL-2) gene
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 <211>
        30
 <212>
       DNA
 <213>
       Artificial
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 <223>
        PCR primer for amplifying the 5'-flanking region of Human interleukin-2
 <400> 28
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                                                                         30
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 〈211〉
〈212〉
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        DNA
 <213> Homo sapiens
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⟨222⟩ (1)...(777)
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        (Acession: HSIL05)
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                                                                         60
tgtacataga cattaagaga cttaaacaga tatataatca ttttaaatta aaatagcgtt
                                                                       120
aaacagtacc tcaagctcaa taagcatttt aagtattcta atcttagtat ttctctagct
                                                                       180
gacatgtaag aagcaatota tottattgta tgcaattago totttgtgtg gataaaaagg
                                                                       240
taaaaccatt ctgaaacagg aaaccaatac acttcctgtt taatcaacaa atctaaacat
                                                                       300
ttattctttt catctgttta ctcttgctct tgtccaccac aatatgctat tcacatgttc
                                                                       360
agtgtagttt tatgacaaag aaaattttct gagttacttt tgtatcccca cccccttaaa
                                                                       420
gaaaggagga aaaactgttt catacagaag gcgttaattg catgaattag agctatcacc
                                                                       480
taagtgtggg ctaatgtaac aaagagggat ttcacctaca tccattcagt cagtctttgg
                                                                       540
gggtttaaag aaattccaaa gagtcatcag aagaggaaaa atgaaggtaa tgttttttca
                                                                       600
gactggtaaa gtotttgaaa atatgtgtaa tatgtaaaac attttgacac ccccataata
                                                                       660
tttttccaga attaacagta taaattgcat ctcttgttca agagttccct atcactcttt
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aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctcctgt
                                                                       777
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       30
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       30
<212>
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      Artificial
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       PCR primer for amplifying the 5'-flanking region of Human interleukin-2
       (IL-2) gene
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 <213>
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(1)..(538)
 <221>
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        (Acession: HSIL05)
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ttattctttt catctgttta ctcttgctct tgtccaccac aatatgctat tcacatgttc
                                                                        120
agtgtagttt tatgacaaag aaaattttct gagttacttt tgtatcccca cccccttaaa
                                                                       180
gaaaggagga aaaactgttt catacagaag gcgttaattg catgaattag agctatcacc
                                                                       240
taagtgtggg ctaatgtaac aaagagggat ttcacctaca tccattcagt cagtctttgg
                                                                       300
                                                                       360
gggtttaaag aaattccaaa gagtcatcag aagaggaaaa atgaaggtaa tgttttttca
gactggtaaa gtotttgaaa atatgtgtaa tatgtaaaac attttgacac coccataata
tttttccaga attaacagta taaattgcat ctcttgttca agagttccct atcactcttt
                                                                       480
aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctcctgtc
                                                                       538
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       32
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       28
⟨212⟩
       DNA
<213>
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                                                                        28
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       33
<211>
       28
⟨212⟩
       DNA
<213>
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<400> 33
ataagctttg gtggttgcgg agggttcg
                                                                        28
<210>
       34
(211)
      28
(212>
      DNA
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<223> PCR primer for amplifying the promoter region of Human GATA-1 gene
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atggtaccac cccagaagat gccaggag
                                                                        28
<210>
      35
〈211〉
      28
<212>
      DNA
⟨213⟩
      Artificial
〈220〉
<223> PCR primer for amplifying the promoter region of Human GATA-1 gene
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<400> 35
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<210> 37
<211> 25
 <212> DNA
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ggagcggccg cttcaggcca acttg
                                                                         25
<210> 38
<211> 24
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<223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene
<400> 38
ggggatccat ggcgtacagt caag
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<210> 39
<211> 29
<212> DNA
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<223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene
<400> 39
ggtgcggccg ccaaattcag gggttgctg
                                                                         29
<210> 40
<211> 22
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(213) Artificial
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<223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene
<400> 40
                                                                        22
ccggatccac catggccaag ac
<210> 41
<211> 28
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(213) Artificial
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<400> 41
gcagcggccg ccactcttaa atctccac
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<210>
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        28
 <212> DNA
        Artificial
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 <220>
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 <213> Artificial
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 aaggogoogo agottogagg gagtgotac
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 <210> 44
 <211> 27
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 (213) Artificial
(223) PCR primer for amplifying a human histone deacetylase-5 (HDAC5) gene
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<210> 45
<211> 29
<212> DNA
⟨213⟩ Artificial
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                                                                      29
<210> 46
<211> 27
<212> DNA
<213> Artificial
(223) PCR primer for amplifying a human histone deacetylase-6 (HDAC6) gene
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gcgaagctta tgacctcaac cggccag
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⟨210⟩
      47
<211>
      33
(212) DNA
(213) Artificial
<220>
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gcatgcggcc gcttagtgtg ggtggggcat atc
                                                                     33
<210> 48
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<211> 26
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        DNA
        Artificial
 <213>
 <220>
 <223> PCR primer for amplifying a human histone deacetylase-7 (HDAC7) gene
 <400> 48
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                                                                        26
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 <211> 26
 <212> DNA
<213> Artificial
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                                                                        26
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<211> 26
 <212> DNA
<213> Artificial
<220>
<223> PCR primer for amplifying a human histone deacetylase-8 (HDAC8) gene
<400> 50
cgaattcttt aagcggaaga tggagg
                                                                        26
⟨210⟩ 51
<211> 26
<212>
      DNA
(213) Artificial
<220>
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aggtaccgac cacatgcttc agattc
<210>
       52
⟨211⟩ 24
<212> DNA
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<220>
<223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene
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ctgaattcac catggccaag accg
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⟨211⟩ 61
⟨212⟩ DN
      DNA
(213) Artificial
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<223> PCR primer for adding a Flag sequence to a human histone deacetylase-3
       (HDAC3) gene
                                                                       60
gggcggccgc ctacttgtca tcgtcgtcct tgtaatcggt accaatctcc acatcgcttt
C
                                                                       61
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<210> 54

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<211> 8
<212> PRT
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 <400> 54
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5
 <210> 55
<211> 31
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 ⟨213⟩ Artificial
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 ⟨223⟩
       PCR primer for adding a Kpn I site to a human histone deacetylase-1
        (HDAC1) gene
 <400> 55
 atoggtaccg gccaacttga cctcctcctt g
                                                                            31
 <210> 56
<211> 29
 <212> DNA
 (213) Artificial
 <220>
 〈223〉
        PCR primer for adding a Kpn I site to a human histone deacetylase-2
        (HDAC2) gene
<400> 56
atcggtaccg gggttgctga gctgttctg
                                                                           29
<210> 57
<211> 27
<212> DNA
⟨213⟩ Artificial
<220>
<223>
       PCR primer for adding a Bgl II site to a human histone deacetylase-4
        (HDAC4) gene
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                                                                           27
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<210> 58
<211> 46
<212> DNA
<213> Artificial
(223) Nucleotide sequence having a Flag nucleotide sequence
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aattootgoa gagatotgat tacaaggacg acgatgacaa gtaggo
                                                                           46
<210> 59
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<212> DNA
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<210>
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        DNA
 〈212〉
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 <223>
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(213) Artificial
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PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene
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⟨211⟩
⟨212⟩
        20
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        Artificial
<213>
<220>
        PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene
⟨223⟩
<400> 62
                                                                                 20
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⟨211⟩
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        PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene
<223>
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       Artificial
<220>
<223>
        PCR primer for creating a dominant negative mutant (H863L) of human
        histone deacetylase-4 (HDAC4) gene
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cctgtacatg tccctccttc g
                                                                                 21
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       65
〈211〉
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       20
       DNA
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        PCR primer for creating a dominant negative mutant (H863L) of human
        histone deacetylase-4 (HDAC4) gene
<400>
        65
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⟨223⟩ PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 70 gacggcgtgg aagaggcctt c

21

<210> 71 <211> 26 (212) DNA <213> Artificial

<220> <223> PCR primer for creating a dominant negative mutant (H199L) of human

(57)

histone deacetylase-1 (HDAC1) gene

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                                                                                   26
 gaagtactct ccatacttaa gaaagg
 <210> 72
 (211) 26
 <212> DNA
 <213> Artificial
        PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene
 ⟨223⟩
<400> 72
ctgtgtcctt tcttaagtat ggagag
                                                                                   26
<210> 73
<211> 22
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        PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene
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                                                                                   22
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<212> DNA
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       Artificial
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        histone deacetylase-3 (HDAC3) gene
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        75
        26
<212> DNA
⟨213⟩ Artificial
<220>
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       PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene
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                                                                                  26
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<220>
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<400> 76
                                                                                  25
tggtggtctg aagcttgcca agaag
<210> 77
<211>
      21
(212)
      DNA
<213> Artificial
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〈220〉
 <223>
        PCR primer for creating a dominant negative mutant (H134K, H135L) of human
         histone deacetylase-3 (HDAC3) gene
 <400> 77
 cccgtcacca tggtggatgt c
                                                                               21
 (210) 78
 <211>
        23
 〈212〉
        DNA
 ⟨213⟩
        Artificial
 <220>

PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase—3 (HDAC3) gene

 <400> 78
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                                                                               23
<210> 79
<211> 26
 <212> DNA
 <213>
        Artificial
 <220>
<223>
        PCR primer for creating a dominant negative mutant (H193L) of human
        histone deacetylase-3 (HDAC3) gene
<400> 79
gaagtaattt ccgtacttaa ggaagg
                                                                               26
<210> 80
<211> 26
<212> DNA
<213> Artificial
<220>
<223>
       PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene
<400> 80
tgtccttcct taagtacgga aattac
                                                                              26
<210> 81
<211>
       22
<212> DNA
<213> Artificial
<220>
<223>
       PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene
<400> 81
gagcacaatg cacgtgggtt gg
                                                                              22
<210> 82
<211>
<212>
       29
       DNA
<213>
      Artificial
<220>
(223) PCR primer for amplifying RD3 sequence of human N-CoR gene
gggatccgtg aagtccttca gcctgctcc
                                                                              29
<210>
⟨211⟩ 29
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<212> DNA
 <213> Artificial
 <220>
        PCR primer for amplifying RD3 sequence of human N-CoR gene
 <223>
 <400> 83
                                                                        29
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 ⟨212⟩⋅
        DNA
 <213> homo sapiens
 〈220〉
 <221>
       misc_feature
(1)..(960)
 <222>
        Corresponding to the sequence (+5281 to +6240) in the GenBank database
 <223>
        (Acession: AF196971)
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                                                                        60
 catcoctggc toccacctca gtttcccgcc tccaaggcag catggcgggc aagaagttga
                                                                       120
                                                                       180
 ggccactgtc cctgggtgtt cctacccca caccctcacc ccaagacagc ctgttactgc
 ggogocaaca gocacggtog cotacatotg ataagactta totgotgoco cagggoaggo
                                                                       240
                                                                       300
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12

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